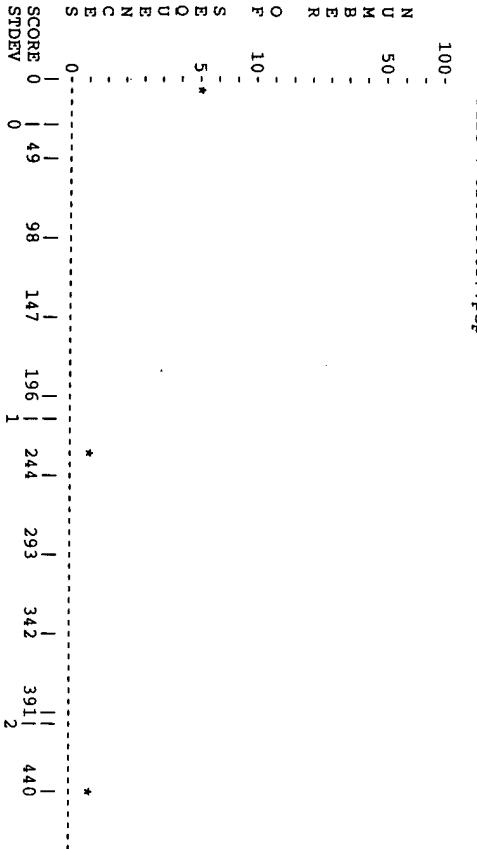```
>O<
O||O   Intelligenetics
>O<

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq1-3_5.res made by mruhl on Wed 22 Jan 103 17:05:36-PST.

Query sequence being compared: US-09-894-657-1 (1-168)
Number of sequences searched: 6
Number of scores above cutoff: 6

            Results of the initial comparison of US-09-894-657-1 (1-168) with:
            File : US09894657.pep
```

```
100-


N
U  50-
M
B
E
R
       *
O      *  .
F  10-
       *
O      * .
F  5-

S
E
Q    . .
U
E
N
C
E
S
  0-
                                                           *
                                                   *    *
SCORE 0    19   37   56   75   93  112  131  149  168
STDEV      |    |    |    |    |    |    |    |    |
           0         1
```

PARAMETERS

```
Similarity matrix    PAM-150
Threshold level of sim.  168%          K-tuple          2
Mismatch penalty         1
Gap penalty              5.00          Joining penalty  20
Gap size penalty         0.05          Window size      168

Cutoff score             1
Randomization group      0
```

SEARCH STATISTICS

	Mean	Median	Standard Deviation
Scores:	60	13	78.39

Times:
```
           CPU                Total Elapsed
00:00:00.00                   00:00:00.00
```

```
Number of residues:                     2027
Number of sequences searched:           6
Number of scores above cutoff:          6
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

```
                                     Init.    Opt.
Sequence Name   Description   Length  Score    Score   Sig.  Frame
```

----

1. US-09-894-657-1 Sequence 1, Application US/09894657

The list of other best scores is:

```
                                     Init.    Opt.
Sequence Name   Description   Length  Score    Score   Sig.  Frame
```

----

1. US-09-894-657-1 (1-168)
   US-09-894-657-1 Sequence 1, Application US/09894657   168   168   168   1.38   0

2. US-09-894-657-7 Sequence 7, Application US/09894657
   **** 1 standard deviation above mean ****
   **** 0 standard deviation from mean ****   168   154   154   1.20   0

3. US-09-894-657-9 Sequence 9, Application US   469   12   81   -0.61   0
4. US-09-894-657-5 Sequence 5, Application US   469   12   81   -0.61   0
5. US-09-894-657-8 Sequence 8, Application US   313   7   76   -0.68   0
6. US-09-894-657-3 Sequence 3, Application US   440   7   76   -0.68   0

```
1. US-09-894-657-1 (1-168)
   US-09-894-657-1 Sequence 1, Application US/09894657

   Initial Score    =  168    Optimized Score  =  168    Significance =  1.38
   Residue Identity =  100%   Matches          =  168    Mismatches   =  0
   Gaps             =  0      Conservative Substitutions   =  0

        10        20        30        40        50        60        70
X   MFQIPEFEPSEQEDSSSAAERGLGPSPAGDGPSGSGGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEIRSR
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    MFQIPEFEPSEQEDSSSAAERGLGPSPAGDGPSGSGGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEIRSR
X        10        20        30        40        50        60        70

        80        90       100       110       120       130       140
HSSYPAGTEDDEDGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDEFVDSFKKGLPRPKSAGTATQMRQS
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
HSSYPAGTEDDEDGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDEFVDSFKKGLPRPKSAGTATQMRQS
        90       100       110       120       130       140

       150       160
SSWTRVFQSWWDRNLGRGSSAPSQ
|||||||||||||||||||||||
SSWTRVFQSWWDRNLGRGSSAPSQ
       150       160     X
```

```
2. US-09-894-657-1 (1-168)
   US-09-894-657-7 Sequence 7, Application US/09894657

   Initial Score    =  154    Optimized Score  =  154    Significance =  1.20
   Residue Identity =  85%    Matches          =  143    Mismatches   =  24
   Gaps             =  0      Conservative Substitutions   =  1

        10        20        30        40        50        60        70
X   MFQIPEFEPSEQEDSSSAAERGLGPSPAGDGPSGSGGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEIRSR
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLMDASHQQEQPTSSSHHGGRWGCGDPES
X        10        20        30        40        50        60        70

        80        90       100       110       120       130       140
HSSYPAGTEDDEDGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDEFVDSFKKGLPRPKSAGTATQMRQS
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
PQLLPRGDGGRRDGGGAQPFRGRSRSAPPNLWAAQRYGRELRRMSDEFVDSFKKGLPRPKSAGTATQMRQS
        90       100       110       120       130       140

       150       160
SSWTRVFQSWWDRNLGRGSSAPSQ
|||||||||||||||||||||||
SSWTRVFQSWWDRNLGRGSSAPSQ
       150       160     X
```

```
3. US-09-894-657-1 (1-168)
   US-09-894-657-9 Sequence 9, Application US/09894657

   Initial Score    =  12     Optimized Score  =  81     Significance = -0.61
```

Residue Identity = 8%   Matches = 15   Mismatches = 141
Gaps = 0   Conservative Substitutions = 12

```
                   10        20        30        40        50        60        70
          DPDNLSDSLFSGDEENAGTEEIKNELNGNWISASTINEARINAKAKRRLRKNSSRDSGRGDSVSDNGSEAVR
                   X                                                        X
                                                           10        20
                                                    MFQIPEFEPSEQEDSSSAAERGL
                                                           X

                   30        40        50        60        70        80        90
          GPSPAGDGPSSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFR
               :|:                                 :|   :  :|:         |:    :|f

                   90       100       110       120       130       140       150
          SGVAVPTSPKGRLLDRRSRSGKGRGLPKKGGAGGKGVWGTPGQVYDVEEVDVKDNYDDDQENCYYETVVLP
                                         X                            |:|
                                                           140       150
                                                      KQQLDPKPQVSGRPPVIKPEVDST

                  100       110       120       130       140       150       160
          GRSRSAPPNLWAAQRYGRELRRMSDEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAP
                   |:|:                                                    |:|:

                  160       170       180       190       200       210       220
          LDETAFEKTLTPIIQEYFEHGDTNEVAEMLRDLNLGEMKSGVPVLAVSLALEGKASHREMTSKLLSDLCGTV
                   X                                                        X
                  290
          EDVHELKKLNLS
```

4. US-09-894-657-5 Sequence 5, Application US/09894657
US-09-894-657-1 (1-168)

Initial Score = 12   Optimized Score = 81   Significance = -0.61
Residue Identity = 8%   Matches = 14   Mismatches = 144
Gaps = 0   Conservative Substitutions = 10

```
                   10        20
            MFQIPEFEPSEQEDSSSAAERGL
                   X         X

                   10        20        30        40        50        60        70
          MSTNDVEKSFDKLLKDLPELALDTPRAPQLVGQFIARAVGDGILCNTYIDSY
                  240       250       260       270       280

                   10        20        30        40        50        60        70
          NEQILNVNPADPDNLSDSLFSGDEENAGTEEVKNELNGNWISASSINEARINAKAKRRLRKRNSSRDSGRGDS
                  10        20        30        40        50        60        70
                                                                            X

                   30        40        50        60        70        80        90
          GPSPAGDGPSSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFR
                                                                            X
                   10        20        30        40        50        60
            MFQIPEFEPSEQEDSSSAAERGLGPSPAGDGPSSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGA
                  80        90       100       110       120       130
          VSDSGSDALRSGLTVPTSPKGRLLDRRSRSGKGRGLPKKGGAGGKGVWGTPGQVYDVEEVDVKDNYDDDQE
                                                                            X

                  100       110       120       130       140       150       160
          GRSRSAPPNLWAAQRYGRELRRMSDEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAP
                                                                    |:|:
                  140       150       160
          AGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ

                  150       160       170       180       190       200       210
          NCVYETVVLPLDERAFEKTLTPIIQEYFEHGDTNEVAEMLRDLNLGEMKSGVPVLAVSLALEGKASHREMTS
                                                                            X
                  150       160
          KEQLDPKPQVSGRPPVIKPEVDSTFCHNYVFPIQTLDCKRKELKKVPNNIPPDIVKLDLSYNKINQLRPKEF
                  220       230       240       250       260       270       280

                  170       180       190       200       210       220
          KLLSDLCGTVMSTTDVEKSFDKLLKDLPELALDTPRAPQLVGQFIARAVGDG
                  230       240       250       260       270
                                                                            X
          EDVHELKKLNLS
                  300
```

5. US-09-894-657-8 Sequence 8, Application US/09894657
US-09-894-657-1 (1-168)

Initial Score = 7   Optimized Score = 76   Significance = -0.68
Residue Identity = 9%   Matches = 22   Mismatches = 143
Gaps = 74   Conservative Substitutions = 3

```
                   10        20        30        40        50        60
            MFQIPEFEPSEQEDSSSAAERGLGPSPAGDGPSSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGA
                   X                                                    X
                   10        20        30        40        50        60        70
          MRVVTIVILLCFCKAAELRKASPGSVSRVNHGRAGGGRRGSNPVKRYAPGLPCDVYTYLHEKYLDCQERKL
                   10        20        30        40        50        60        70
```

6. US-09-894-657-3 Sequence 3, Application US/09894657
US-09-894-657-1 (1-168)

Initial Score = 7   Optimized Score = 76   Significance = -0.68
Residue Identity = 12%   Matches = 24   Mismatches = 135
Gaps = 19   Conservative Substitutions = 9

```
                   70        80        90       100
          GAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQ-----------------------------
                   80        90       100       110       120       130
          VYVLPGWPQDLLHMLLARNKIRTLKNNMFSKFKLKSLDLQQNEISKIESEAFFGLNKLTTLLLQHNQIKVL
                  80        90       100
                                                           110       120       130
                                                      RYGRELRRMSDEFVDSFKKGLPRPKS
                  140       150       160       170       180       190
          TEEVFIYTPLLSYLRLYDNPWHCTCEIETLISMLQIPRNRNLANYAKCESPQEQKNKKLRQIKSEQLCNEEK
                  150       160       170       180       190       200
          AGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ
                                                                            X
          EDVHELKKLNLS
```

6. US-09-894-657-3 Sequence 3, Application US/09894657
US-09-894-657-1 (1-168)

Initial Score = 7   Optimized Score = 76   Significance = -0.68
Residue Identity = 12%   Matches = 24   Mismatches = 135
Gaps = 19   Conservative Substitutions = 9

```
                   10        20        30        40        50        60
            MFQIPEFEPSEQEDSSSAAERGLGPSPAGDGPSSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGA
                   X         X                                           X
                   10        20        30        40        50        60        70
          MRVVTIVILLCFCKAAELRKASPGSVSRVNHGRAGGGRRGSNPVKRYAPGLPCDVYTYLHEKYLDCQERKL
                   10        20        30        40        50        60        70

                   70        80        90       100
          GAV--------------EIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRM
                                        :|     ||  |  ::|           :
          VVYLPGWPQDLLHMLLARNKIRTLKNNMFSKFKLKSLDLQQNEISKIESEAFFGLNKLTTLLLQHNQIKVL
                  80        90       100       110       120       130       140

                  120       130       140       150       160
          SDEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ
                   :|                ||:||      :   ||||       :
          TEEVFIYTPLLSYLRLYDNPWHCTCEIETLISMLQIPRNRNLGNYAKCESPQEQKNKKLRQIKSEQLCNEEK
                  150       160       170       180       190       200       210
          EQLDPKPQVSGRPPVIKPEVDSTFCHNYV
                  220       230       240
```

```
> O <
OI |O    IntelliGenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq3-5.res made by mruhl on Wed 22 Jan 103 17:09:59-PST.

Query sequence being compared:US-09-894-657-3 (1-440)
Number of sequences searched: 6
Number of scores above cutoff: 6

Results of the initial comparison of US-09-894-657-3 (1-440) with:
    File : US09894657.pep

```
  N
U 100-
M
B
E  50-
R

O
F  10-

S   5-*
E
Q
U
E
N   0-
C
E   |---|---|---|---|---|---|---|---|---|---|
S  SCORE 0   49  98  147 196 244 293 342 391 440
   STDEV 0    1        *                 1   2
                    1   1                    2
```

```
                        PARAMETERS
Similarity matrix       PAM-150
Threshold level of sim. 16%
Mismatch penalty        1        K-tuple           2
Gap penalty             5.00     Joining penalty   1
Gap size penalty        0.05     Window size       20
Cutoff score            1                          440
Randomization group     0
```

```
                SEARCH STATISTICS
                Mean    Median
Scores:         116     9.

                Standard Deviation
                181.57
```

```
Times:
        CPU            Total Elapsed
    00:00:00.00        00:00:00.00
```

Number of residues: 2027
Number of sequences searched: 6
Number of scores above cutoff: 6

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name   Description   Length Init.   Opt.   Sig. Frame
                                                Score   Score

---

1. US-09-894-657-3 Sequence 3, Application US 09894657   440   440   440   1.78   0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
2. US-09-894-657-8	Sequence 8, Application US	313	229	305	0.62	0
3. US-09-894-657-9	Sequence 9, Application US	469	8	184	-0.59	0
4. US-09-894-657-5	Sequence 5, Application US	469	8	185	-0.59	0

1. US-09-894-657-3 (1-440)
   US-09-894-657-3 Sequence 3, Application US/09894657

```
Initial Score    =  440    Optimized Score   =  440    Significance =  1.78
Residue Identity =  100%   Matches           =  440    Mismatches   =  0
Gaps             =  0      Conservative Substitutions =  0
```

```
X
        10        20        30        40        50        60        70
MRVVTIVILLCFCKAAELRKASPGSVRSRVNHGRAGGGRRGSNPVKRYAPGLPCDVYTYLHEKYLDCQERKL
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MRVVTIVILLCFCKAAELRKASPGSVRSRVNHGRAGGGRRGSNPVKRYAPGLPCDVYTYLHEKYLDCQERKL
X
        10        20        30        40        50        60        70

        80        90       100       110       120       130       140
VYVLPGWPQDLLHMLLARNKIRTLKNNMFSKFKKLKSLDLQQNEISKIESEAFPGLNKLTTLLLQHNQIKVL
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
VYVLPGWPQDLLHMLLARNKIRTLKNNMFSKFKKLKSLDLQQNEISKIESEAFPGLNKLTTLLLQHNQIKVL
        80        90       100       110       120       130       140

       150       160       170       180       190       200       210
TEEVFIYTPLLSYLRLYDNPWHCTCEIETLISMLQIPRNRNLGNYAKCESPQEQOKNKKLRQIKSEQLCNEEK
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TEEVFIYTPLLSYLRLYDNPWHCTCEIETLISMLQIPRNRNLGNYAKCESPQEQOKNKKLRQIKSEQLCNEEK
       150       160       170       180       190       200       210

       220       230       240       250       260       270       280
EQLDPKPQVSGRPPVIKPEVDSTPFCHNYVFPIQTLDCKRKELKKVPNNIPPDIVKLDLSYNKINQLRPKEFE
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
EQLDPKPQVSGRPPVIKPEVDSTPFCHNYVFPIQTLDCKRKELKKVPNNIPPDIVKLDLSYNKINQLRPKEFE
       220       230       240       250       260       270       280

       290       300       310       320       330       340       350       360
DVHELKKLNLSSNGIEFIDPAAFLGLTFHLEEDLDLSNNSLQNFDYGVLEDLYFLKLLWLRDNPWRCDYNHYL
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DVHELKKLNLSSNGIEFIDPAAFLGLTFHLEEDLDLSNNSLQNFDYGVLEDLYFLKLLWLRDNPWRCDYNHYL
       290       300       310       320       330       340       350       360

       370       380       390       400       410       420       430
YYWLKHHYNVHFNGLECKTPEEYKGWSVGKYIRSYYEECPKDKLPAYPESFDQDTEDDEWEKKIHRDHTAKKQ
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
YYWLKHHYNVHFNGLECKTPEEYKGWSVGKYIRSYYEECPKDKLPAYPESFDQDTEDDEWEKKIHRDHTAKKQ
       370       380       390       400       410       420       430

       440
SVIITIVG
||||||||
SVIITIVG
       440
```

2. US-09-894-657-3 (1-440)
   US-09-894-657-8 Sequence 8, Application US/09894657

```
Initial Score    =  229   Optimized Score   =  305   Significance =  0.62
Residue Identity =  98%   Matches           =  307   Mismatches   =  2
Gaps             =  1     Conservative Substitutions =  3
```

```
X
        10        20        30        40        50        60        70
MRVVTIVILLCFCKAAELRKASPGSVRSRVNIGRAGGGRRGSNPVKRYAPGLPCDVYTYLHEKYLDCQERKL
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
X
MRVVTIVILLCFCKAAAELRKASPGSVRSRVNHGRAGGGRRGSNPVKRYAPGLPCDVYTYLHEKYLDCQERKL
    10        20        30        40        50        60        70

X
VYVLPGWPQDLLHMLLARNKIRTLKNNMFSKFKFKLKSLDLQQONEISKIESEAFFGINKLTTLLLQHNQIKVL
||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
VYVLPGWPQDLLHMLLARNKIRTLKNNMFSKFKLKSLDLQQONEISKIESEAFFGINKLTTLLLQHNQIKVL
    80        90        100       110       120       130       140

TEEVFIYTPLLSYLRLYDNPWHCTCEIETLLISMLQIPRNRNLGN
|||||||||||||||||||||||||||||||||||:|:
TEEVFIYTPLLSYLRLYDNPWHCTCEIETLLISMLQIPRNRNLANYAKCESPQEQKNKKLRQIKSEQLCN-EE
    150       160       170       180       190       200       210

KEQLDPKPQVSGRPPVIKPEVDSTFCHNYVFPIQTLDCKRRELKKYVPNNIPPDIVKLDLSYNKINQLRPKEF
|||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
KEQLDPKPQVSGRPPVIKPEVDSTFCHNYVFPIQTLDCKRKELKKYVPNNIPPDIVKLDLSYNKINQLRPKEF
    220       230       240       250       260       270       280

EDVHELKKLNLSSNGIEFIDPAAFLGLTHLEELDLSNNSLQNFDYGVLEDLYFLKLLWLRDNPWRCDYNIHY
||||||||||||||||||||||||||||||:::
EDVHELKKLNLSSNGIEFIDPGSLR
    290       300       310        X
```

3. US-09-894-657-3 (1-440)
   US-09-894-657-9 Sequence 9, Application US/09894657

```
Initial Score     = 8    Optimized Score         = 184   Significance = -0.59
Residue Identity   = 8%   Matches                 = 37    Mismatches   = 379
Gaps              = 13   Conservative Substitutions = 24
```

```
         360
         LYY
```

```
X
MRVVTIVILLCFCKAAAELRKASPGSVRSRVNHGRAGGGRRGSNPVKRYAPGLPCDVY
    10        20        30        40        50

MDIENEQTLNVNPTDPDNLSDSLFSGDEENAGTEEIKNEINGNWISASTINEARINAKAKRLRKNSSRDSG
    10      X 20        30        40        50        60        70

TYLHEKYLDCQERKLVYVLPGWPQD-LLHMLLARNKIRTLKNNMFSKFKFKLKSLDLQQONEISKIESEA----
    60        70        80        90        100       110       120
  :.         :: |   ||||||||||||||||||| :
RGDSVSDNGSEAVRSGVAVPTSPKGRLLDRRSRSGKGRGLPKKGGAGGKGVWGTPGQVYDVEEVDVKDPNYD
    80        90        100       110       120       130       140

--------FFGLNKLTTLLLQHNQIKVLTEEVFIYTPLLSYLRLYDNPWHCTCEIETLLISMLQIPRNRLGN
    130       140       150       160       170       180
        :.
DDQENCVYETVVLPLDETAFERKTLTPIIQEYFEHGDTNEVAEMLRDLNLGEMKSGVPVLAVSLALEGKASHR
    150       160       170       180       190       200       210

YAKCESPQEQKNKKLRQIKSEQLCNEEKEQLDPKPQVSGRPPVIKPEVDSTFCHNYVFPIQTLDCKRKELKK
    190       200       210       220       230       240       250       260

EMTSKLLSDLCGTVMSTNDVEKSFDKLLKDLPELALDTPRAPQLVGQFIARAVGDGILCNTYIDSYKGTVDC
    220       230       240       250       260       270       280

VPNNIPPDIVKLDLSYNKINQLRPKEFEDVHELKKLNLSSNGIEFIDPAAFLGLTHLEELDLSNNSLQNFDY
    270       280       290       300       310       320       330

VQARAALDKATVLLSMSKGGKRRDSVWGSGGGQQPVNHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFH
    290       300       310       320       330       340       350       360

HELVYEAIVMVLESTGESAFKMILDLLKSLWKSSTITIDDQMKRGYERIYNEIPDINLDVPHSYSVLERFVEE
    340       350       360       370       380       390       400

CFQAGIISKQLRDLCPSRGRKRFVSEGDGGRLKPESY
    410       420       430       440      X

PAYPESFDQDTEDDEWEKKHRDHTAKKQSVIITIVG
    410       420       430       440
```

4. US-09-894-657-3 (1-440)
   US-09-894-657-5 Sequence 5, Application US/09894657

```
Initial Score     = 8    Optimized Score         = 185   Significance = -0.59
Residue Identity   = 8%   Matches                 = 38    Mismatches   = 379
Gaps              = 13   Conservative Substitutions = 23
```

```
X
MRVVTIVILLCFCKAAAELRKASPGSVRSRVNHGRAGGGRRGSNPVKRYAPGLPCDVY
    10        20        30        40        50

MDVENEQILNVNPADPDNLSDSLFSGDEENAGTEEVKNEIGNWISASSINEARINAKAKRRLRKNSSRDSG
    10      X 20        30        40        50        60        70

TYLHEKYLDCQERKLVYVLPGWPQD-LLHMLLARNKIRTLKNNMFSKFKFKLKSLDLQQONEISKIESEA----
    60        70        80        90        100       110       120
  :.         :: |   ||||||||||||||||||| :
RGDSVSDSGSSDALRSGLTVPTSPKGRLLDRRSRSGKGRGLPKKGGAGGKGVWGTPGQVYDVEEVDVKDPNYD
    80        90        100       110       120       130       140

--------FFGLNKLTTLLLQHNQIKVLTEEVFIYTPLLSYLRLYDNPWHCTCEIETLLISMLQIPRNRLGN
    130       140       150       160       170       180
        :.
DDQENCVYETVVLPLDERAFEKTLTPIIQEYFEHGDTNEVAEMLRDLNLGEMKSGVPVLAVSLALEGKASHR
    150       160       170       180       190       200       210

YAKCESPQEQKNKKLRQIKSEQLCNEEKEQLDPKPQVSGRPPVIKPEVDSTFCHNYVFPIQTLDCKRKELKK
    190       200       210       220       230       240       250       260

EMTSKLLSDLCGTVMSTTNDVEKSFDKLLKDLPELALDTPRAPQLVGQFIARAVGDGILCNTYIDSYKGTVDC
    220       230       240       250       260       270       280

VPNNIPPDIVKLDLSYNKINQLRPKEFEDVHELKKLNLSSNGIEFIDPAAFLGLTHLEELDLSNNSLQNFDY
    270       280       290       300       310       320       330

VQARAALDKATVLLSMSKGGKRKDSVWGSGGGQQPVNHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFH
    290       300       310       320       330       340       350       360

HELVYEAIIMVLESTGESTFKMILDLLKSLWKSSTITVDQMKRGYERIYNEIPDINLDVPHSYSVLERFVEE
    340       350       360       370       380       390       400

CFQAGIISKQLRDLCPSRGRKRFVSEGDGGRLKPESY
    410       420       430       440      X

PAYPESFDQDTEDDEWEKKHRDHTAKKQSVIITIVG
    410       420       430       440
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